# **Publishing Dataset to GGBN Protocol**

## Step 1. Downloading the dataset

Tissue and associated specimen data is stored within the Research Department Database.

Navigate to <a href="https://research.botanicgardens.org">https://research.botanicgardens.org</a> and log in.

Once logged in, navigate to <a href="https://research.botanicgardens.org/admin/query.php">https://research.botanicgardens.org/admin/query.php</a> (just add query.php to end of home page web address)

Paste the query from the box below into the web page's box and select "submit"

```
SELECT CONCAT("Tissue ", wd.work_id, "-", wid.work_individual_data_id) AS "catalogNumber", wid.UUID AS "materialSampleID", "Tissue and DNA Bank" AS "collectionCode", "DBG" AS "institutionCode",
"MaterialSample" AS "basisOfRecord", wid.collection_type AS "materialSampleType", dprep.preparationType AS "preparationType", tw.preservation AS "preservationType", pmts.permit_availability AS
"permitStatus", pmtt.permit_type AS "permitType", "For full permit text, please contact Denver Botanic Gardens Research and Conservation directly" AS "permitText", vw.collector_number AS
"recordNumber", u.fullname AS "recordedBy", wd.date_collected AS "eventDate", cntryiso.lsoCode AS "countryCode", cntryiso.Country AS "country", wd.latitude AS "decimalLatitude", sts.state AS
"stateProvince", cnts.county AS "county", wd.longitude AS "decimalLongitude", wd.elevation AS "minimumElevationInMeters", f.family AS "family", sl.synonym_species_name AS "scientificName",
SUBSTRING_INDEX(sl.synonym_species_name, '', 1) AS "genus", SUBSTRING_INDEX(SUBSTRING_INDEX(sl.synonym_species_name, '', 2), ',-1) AS "specificEpithet", "species" AS "taxonRank",
vw.KHD_accession_number AS "catalogNumberVoucher", vw.voucher_GUID AS "occurrenceID", wd.specific_locality AS "locality", "same population" AS "relationshipOfResource"
CONCAT ("catalogNumber=", vw.KHD\_accession\_number, "\&institutionCode=KHD\&collectionCode=vascular and the context of the cont
plants&accessPoint=http://ipt.vertnet.org:8080/ipt/archive.do?r=khd_vascular&guid=",vw.voucher_GUID) AS "resourceRelationshipID", wid.UUID AS "resourceID", vw.voucher_GUID AS "relatedResourceID",
"tissue from many individuals collected from same population as individual taken as voucher specimen" AS "relationshipRemarks", "Permit is available" AS "permitStatusQualifier", wd.date_collected AS
"preparationDate", acsp.redact_locality
FROM work_done AS wd
LEFT JOIN work individuals AS wi ON wd.work id = wi.work id
LEFT JOIN work individual data AS wid ON wi.work individual id = wid.work individual id
LEFT JOIN tissue work AS tw ON wd.work id = tw.work id
LEFT JOIN agencies AS agen ON wd.agency_id = agen.agency_id
LEFT JOIN dna_preparations AS dprep ON tw.preparation_type = dprep.preparation_id
LEFT JOIN permits AS pmts ON wd.permit_id = pmts.permit_id
LEFT JOIN permit types AS pmtt ON pmts.permit type id = pmtt.permit type id
LEFT JOIN countryisocode AS cntryiso ON wd.ID_Country = cntryiso.ID_Country
LEFT JOIN states AS sts ON wd.state id = sts.state id
LEFT JOIN counties AS cnts ON wd.county_id = cnts.county_id
LEFT JOIN voucher work AS vw ON wd.work id = vw.work id
LEFT JOIN users AS u ON vw.primary collector = u.user id
LEFT JOIN work_landowners AS wlndo ON wd.work_id = wlndo.work_id
LEFT JOIN landowners AS Indo ON windo.landowner id = Indo.landowner id
LEFT JOIN accepted_species AS acsp ON wd.accepted_species_id = acsp.accepted_species_id
LEFT JOIN families AS f ON acsp.family id = f.family id
LEFT JOIN synonym_list AS sl ON wd.accepted_species_id = sl.accepted_species_id
WHERE NOT wid.collection type = "herbarium" AND NOT wid.collection type = "seed" AND NOT wid.collection type = "dna" AND wid.collection type IS NOT NULL AND wid.material remaining = 1 AND
vw.work id IS NOT NULL
GROUP BY wid LILLID
```

On the results page, select "Download as CSV"

Locate and open the .csv file that was downloaded.

# Step 2. Checking and modifying the dataset

In order to continue, herbarium specimens must be curated to the point that they have been assigned a catalog number (barcode). If catalogNumberVoucher is blank, these samples are not ready to be published on GGBN.

Check each column for empty records or missing data. If data is missing, contact database associate. In this case, it is likely that default values or pieces of data were not populated during the processing of samples and specimens.

Fields that are commonly left blank, but should be populated within the database (not just in the spreadsheet) include:

- permitStatus
- permitType
- countryCode
- country
- locality
- minimumElevationInMeters

These fields are not included in the initial data entry stages and require secondary action. Contact database associate to do so.

**IMPORTANT** The last column is called redact\_locality. Sort the dataset by this column, from greatest to lowest value. For all records that have the value "1" recorded in redact\_locality, delete the decimalLatitude and decimalLongitude before publication.

Save the file here: Q:\Research\Data Management\GGBN\Published to GGBN

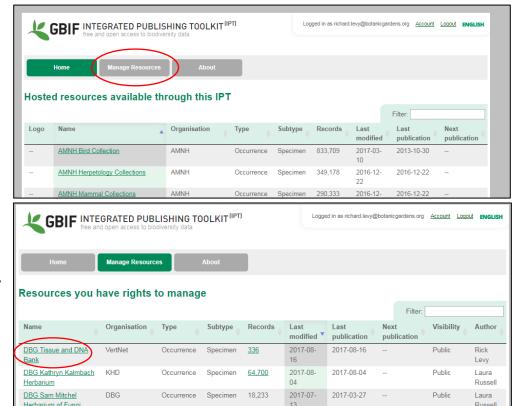
Use the naming convention YYYYMMDD\_dataset\_DBGTissueAndDNABank\_GGBN

#### Step 3. Uploading the file

Navigate to VertNet's IPT instance and log in. Users will need to contact VertNet for access.

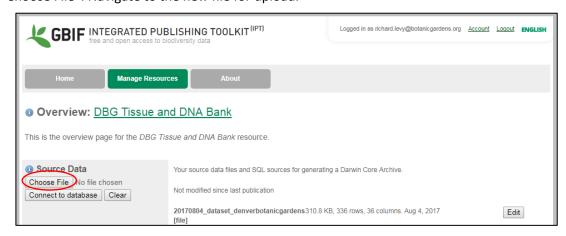
http://ipt.vertnet.org:8080/ipt/

Select "Manage Resources"

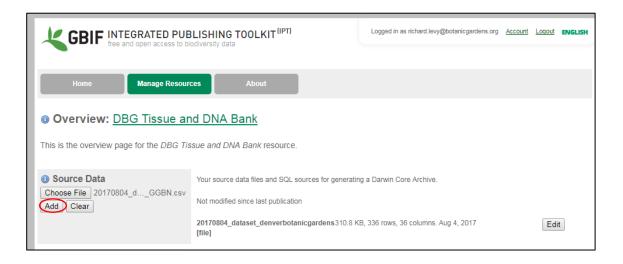


Select "DBG Tissue and DNA Bank"

Under "Source Data" select "Choose File". Navigate to the new file for upload.

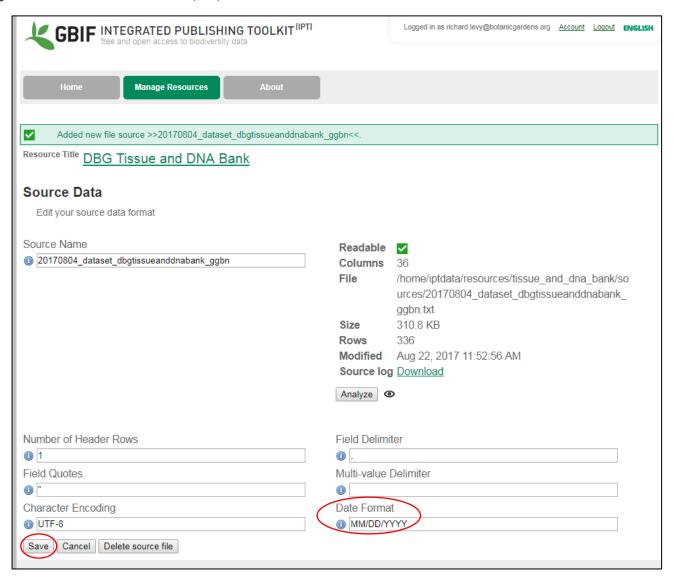


Once the Source File has been selected, select "Add".



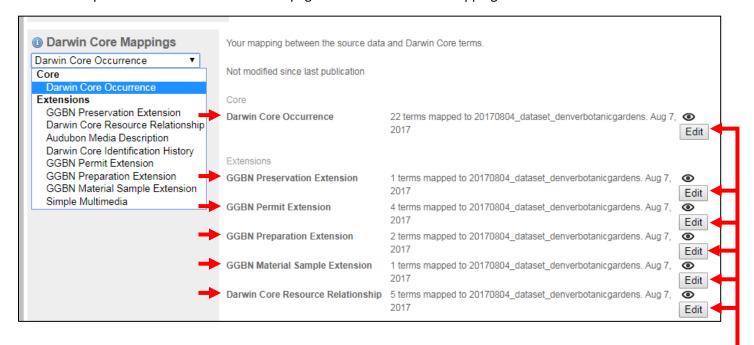
After clicking "add" the user is brought to the Edit Source Data Format page.

Change the "Date Format" to be "MM/DD/YYYY". Then select "Save".



## Step 4. Mapping the Fields

In addition to the Darwin Core Occurrence, 5 Extensions should be added for mapping. They can be selected and added from the dropdown list on the left side of the page under "Darwin Core Mappings".



For each set of mappings, the user must manually map the fields from the original dataset to the accepted term. Select the "Edit" button to the right of each mapping to do so.

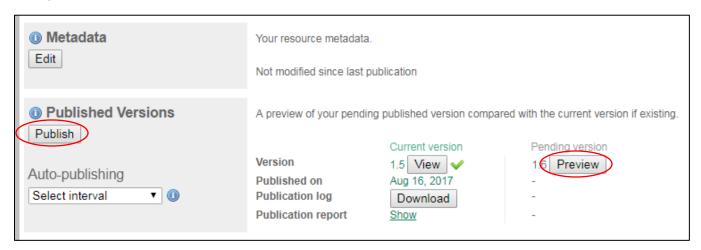
## Map the following fields

Darwin Core Occurrence:			GGBN Preservation Extension		
occurrenceID	$\rightarrow$	materialSampleID	occurrenceID	$\rightarrow$	materialSampleID
institutionCode	$\rightarrow$	institutionCode	preservationType	$\rightarrow$	preservation
collectionCode	$\rightarrow$	collectionCode			
basisOfRecord	$\rightarrow$	basisOfRecord	<b>GGBN Permit Extension</b>		
materialSampleID	$\rightarrow$	materialSampleID	occurrenceID	$\rightarrow$	materialsampleID
catalogNumber	$\rightarrow$	catalogNumber	permitType	$\rightarrow$	permitType
recordNumber	$\rightarrow$	recordNumber	permitStatus	$\rightarrow$	permitStatus
recordedBy	$\rightarrow$	recordedBy	permitStatusQualifier	$\rightarrow$	permitStatusQualifier
eventDate	$\rightarrow$	eventDate	permitText	$\rightarrow$	permitText
country	$\rightarrow$	country			
countryCode	$\rightarrow$	countryCode	GGBN Preparation Extension	on	
stateProvince	$\rightarrow$	stateProvince	occurrenceID	$\rightarrow$	materialSampleID
county	$\rightarrow$	county	preparationType	$\rightarrow$	preparationType
locality	$\rightarrow$	locality	preparationDate	$\rightarrow$	preparationDate
minimumElevationInMeter → minimumElevationInMeters					
decimalLatitude	$\rightarrow$	decimalLatitude	GGBN Material Sample Extension		
decimalLongitude	$\rightarrow$	decimalLongitude	occurrenceID	$\rightarrow$	materialSampleID
scientificName	$\rightarrow$	scientificName			
family	$\rightarrow$	family	Darwin Core Resource Relationship		
genus	$\rightarrow$	genus	occurrenceID	$\rightarrow$	materialSampleID
specificEpithet	$\rightarrow$	specificEpithet	resourceRelationshipID	$\rightarrow$	resourceRelationshipID
taxonRank	$\rightarrow$	taxonRank	relatedResourceID	$\rightarrow$	relatedResourceID
			relationship Of Resource	$\rightarrow$	relationshipOfResource
			relationshipRemarks	$\rightarrow$	relationshipRemarks
			scientificName	$\rightarrow$	scientificName

# Step 5. Preview and Publish the Pending Version

Preview the pending version by selecting "Preview". Verify that everything looks correct.

Once previewed and verified, select "Publish".



Once the user selects "Publish" a window opens a prompt. In the window briefly summarize what has changed in the new version to be published. Then select "Yes" when you are ready to publish. On the next page that opens, the IPT will run through the publishing process and notify the user when it has finished successfully.

